Claims

1. A method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising
   i) providing a compound capable of interacting with the receptor and/or polypeptide thereby interfering with said receptor and said polypeptide interaction,
   ii) presenting the compound of step (i) to the at least two different proteins.

2. The method according to claim 1, wherein the at least two proteins are heterologous.

3. The method according to claims 1 or 2, wherein at least one of the at least two proteins comprises at least two immunoglobulin (Ig)-like domains and/or at least two fibronectin type 3 (F3) domains, or at least one Ig-like and one F3 domain.

4. The method according to claim 1, wherein the cell-surface receptor is selected from the family of fibroblast growth factor receptors (FGFRs) comprising FGFR1, FGFR2, FGFR3 and FGFR4.

5. The method according to claim 4, wherein the fibroblast growth factor receptor is FGFR1 having the amino acid sequence set forth in Swiss-Prot Seq Nos: Q9QZM7, Q99AVV7, Q9UD50 or Q63827, or fragments, or variants thereof, or a functional homologue of said receptor.

6. The method according to claim 1, wherein the polypeptide is selected from the group comprising transmembrane, cell-surface-associated, extracellular matrix-associated and soluble proteins.

7. The method according to claims 1 or 6, wherein the polypeptide is selected from the group comprising cell adhesion molecules, cell-surface receptors, heparan sulphate proteoglycans, metalloproteases, extracellular matrix molecules and growth factors.

8. The method according to the claim 7, wherein the cell adhesion molecule is selected from the group comprising
- Neural Cell Adhesion Molecule (NCAM) (Swiss-Prot Ass. Nos: P13591, P13595-01, P13595),
- Neural cell adhesion molecule L1 (Swiss-Prot Ass. Nos: Q9QYQ7, Q9QY38, P11627, Q05695, P32004),
- Neural Cell Adhesion Molecule-2 (NCAM-2) (Swiss-Prot Ass. No: P36335)
- Neuron-glia Cell Adhesion Molecule (Ng-CAM) (Swiss-Prot Ass. No: Q03696; Q90933),
- Neural cell adhesion molecule CALL (Swiss-Prot Ass. No: O00533),
- Neuroglian (Swiss-Prot Ass. No: P91767, P20241),
- Nr-CAM (HBRAVO, NRCAM, NR-CAM 12) (Swiss-Prot Ass. Nos: Q92823, O15179, Q9QVN3
- Axonin-1/TAG-1 (Swiss-Prot Ass. Nos: Q02246, P22063, P28685),
- Axonal-associated Cell Adhesion Molecule (AxCAM) (NCBI Ass. No: NP_031544.1; Swiss-Prot Ass. No: Q8TC35),
- Myelin-Associated Glycoprotein (MAG) (Swiss-Prot Ass. No: P20917),
- Neural cell adhesion molecule BIG-1 (Swiss-Prot Ass. No: Q62682),
- Neural cell adhesion molecule BIG-2 (Swiss-Prot Ass. No: Q62845),
- Fasciclin (FAS-2) (Swiss-Prot Ass. No: P22648),
- Neural cell adhesion molecule HNB-3/NB-3 (Swiss-Prot Ass. Nos: Q9UQ52, P97528, Q9JMB8)
- Neural cell adhesion molecule HNB-2/NB-2 (Swiss-Prot Ass. Nos: O94779, P07409, P97527),
- Cadherin (Swiss-Prot Ass. No: Q9VW71),
- Junctional Adhesion Molecule-1 (JAM-1) (Swiss-Prot Ass. Nos: Q9JKD5, O88792),
- Neural cell adhesion F3/F11(Contactin) (Swiss-Prot Ass. Nos: Q63198, P1260, Q12860, Q28106, P14781, O93250),
- Neurofascin (Swiss-Prot Ass. Nos: Q90924, Q91Z60; O42414),

- B-lymphocyte cell adhesion molecule CD22 (Swiss-Prot Ass. Nos: Q9R094, P20273),
- Neogenin (NEO1) (Swiss-Prot Ass. Nos: Q92859, P97603, Q90610, P97798),
- Intercellular Cell Adhesion Molecule-5 (ICAM-5/telencephalin) (Swiss-Prot Ass. Nos: Q8TAM9, Q60625) or
- Galactose binding lectin-12 (galectin-12) (Swiss-Prot Ass. Nos: Q91VD1, Q9JKX2, Q9NZ03),
- Galactose binding lectin-4 (galectin-4) (Swiss-Prot Ass. No: Q8K419; P38552),

or fragments, or variants thereof.

9. The method according to the claim 7, wherein the functional cell-surface receptor is selected from the group comprising
- Fibroblast Growth Factor Receptor 1 (FGFR1) (Swiss-Prot Ass. Nos: Q9QZM7, Q99AVV7, Q9UD50, Q63827),
- Fibroblast Growth Factor Receptor 2 (FGFR2) (Swiss-Prot Ass. Nos: Q96KM2, P21802, Q63241),
- Fibroblast Growth Factor Receptor 3 (FGFR3) (Swiss-Prot Ass. Nos: Q95M13, AF487554, Q99052),
- Fibroblast Growth Factor Receptor 4 (FGFR4) (Swiss-Prot Ass. No: Q91742),
- Neurotrophin Tyrosin Kinase Type-2 (NTRKT-2) (Swiss-Prot Ass. No: Q8WXJ5),
- Leukocyte Antigen Related Protein-Tyrosine Phosphatase (LAR-PTPRF) (Swiss-Prot Ass. Nos: Q9EQ17, Q64605, Q64604, Q9QW67, Q9VIS8 P10586),
- Nephrin (Swiss-Prot Ass. Nos: Q925S5, Q9JIX2, Q9ET59, Q9R044, Q9QZS7, Q06500),
- Protein-Tyrosine Phosphatase Receptor type S (PTPRS) (Swiss-Prot Ass. Nos: Q64699, Q13332, O75870),
- Protein-Tyrosine Phosphatase Receptor type kappa (R-PTP-kappa) (Swiss-Prot Ass. No: Q15262),
- Protein-Tyrosine Phosphatase Receptor type D (PTPRD) (Swiss-Prot Ass. Nos: Q8WX65, Q9IAJ1, P23468, Q64487),
- Ephrin type-A receptor 8 (EPHA8/Tyrosine-Protein Kinase Receptor EEK) (Swiss-Prot Ass. Nos: O09127, P29322),
- Ephrin type-A receptor 3 (EPHA8/Tyrosine-Protein Kinase Receptor ETK-

1/CEK4) (Swiss-Prot Ass. No: P29318),
- Ephrin type-A receptor 2 (Swiss-Prot Ass. No: Q8N3Z2)
- Insulin Receptor (IR) (Swiss-Prot Ass. No: Q9PWN6)
- Insulin-like Growth Factor-1 Receptor (IGF-1) (Swiss-Prot Ass. Nos: Q9QVW4, P08069, P24062, Q60751, P15127, P15208)
- Insulin-related Receptor (IRR) (Swiss-Prot Ass. No: P14616),
-Tyrosine-Protein Kinase Receptor Tie-1 (Swiss-Prot Ass. Nos: 06805, P35590, Q06806),
- Roundabout receptor-1 (robo-1) (Swiss-Prot Ass. Nos: O44924, AF041082, Q9Y6N7),
- Neuronal nicotinic acetylcholine receptor alpha 3 subunit (CHRNA3) (Swiss-Prot Ass. Nos: Q8VHH6, P04757, Q8R4G9, P32297)
- Neuronal acetylcholine receptor alpha 6 subunit (Swiss-Prot Ass. Nos: Q15825, Q9R0W9)
- Platelet-Derived Growth Factor Receptor Beta (PDGFRB) (Swiss-Prot Ass. Nos: Q8R406, Q05030),
- Interleukin-6 Receptor (IL-6R) (Swiss-Prot Ass. No: Q00560),
- Interleukin-23 Receptor (IL-23R) (Swiss-Prot Ass. No: AF461422),
- Beta-common cytokine receptor of IL-3, IL5 and GmCsf (Swiss-Prot Ass. No: P32927)
- Cytokine Receptor-Like molecule 3 (CRLF1) (Swiss-Prot Ass. No: Q9JM58),
- Class I Cytokine Receptor (ZCYTOR5) (Swiss-Prot Ass. No: Q9UHH5)
- Netrin-1 receptor DCC (Swiss-Prot Ass. No: P43146),
- Leukocyte Fc Receptor-like Protein (IFGP2) (Swiss-Prot Ass. Nos: Q96PJ6, Q96KM2),
- Macrophage Scavenger Receptor 2 (MSR2) (Swiss-Prot Ass. No: Q91YK7), or
- Granulocyte Colony Stimulating Factor Receptor (G-CSF-R) (Swiss-Prot Ass. No: Q99062),

or fragments, or variants thereof.

10. The method according to the claim 7, wherein the heparan sulphate proteoglycan is perlecan (Swiss-Prot Ass. No: P98160), or a fragment, or a variant thereof.

11. The method according to the claim 7, wherein the metalloprotease is selected from the group comprising

- - ADAM-8 (Swiss-Prot Ass. No: Q05910),
- ADAM-19 (Swiss-Prot Ass. Nos: Q9H013, O35674),
- ADAM-8 (Swiss-Prot Ass. No: P78325),
- ADAM-12 (Swiss-Prot Ass. Nos: O43184, Q61824),
- ADAM-28 (Swiss-Prot Ass. Nos: Q9JLN6, Q61824, Q9XSL6, Q9UKQ2),
- ADAM-33 precursor (Swiss-Prot Ass. Nos: Q8R533, Q923W9),
- ADAM-9 (Swiss-Prot Ass. Nos: Q13433, Q61072),
- ADAM-7 (Swiss-Prot Ass. NoS: Q9H2U9, O35227, Q63180),
- ADAM-1A Fertilin alpha (Swiss-Prot Ass. No: Q8R533),
- ADAM-15 (Swiss-Prot Ass. Nos: Q9QYV0, O88839, Q13444),
- Metalloproteinase-desintegrin domain containing protein (TECAM) (Swiss-Prot Ass. No: AF163291),
- Metalloproteinase 1 (Swiss-Prot Ass. Nos: O95204, Q9BSI6),

or fragments, or variants thereof.

12. The method according to the claim 7, wherein the extracellular matrix molecule is selected from the group comprising

- Collagen type VII (Swiss-Prot Ass. No: Q63870),
- Fibronectin (Swiss-Prot Ass. Nos: Q95KV4, Q95KV5, P07589, Q28377, U42594, O95609, P11276), or
- Tenascin-R (Swiss-Prot Ass. Nos: Q15568, O00531, Q90995, P10039),

or fragments, or variants thereof.

13. The method according to the claim 7, wherein the growth factor is Cytokine-like factor-1 (CLF-1) (Swiss-Prot Ass. No:O75462), or a fragment, or a variant thereof.

14. The method according to claim 1, wherein the interaction between the at least two different proteins is a low affinity interaction.

15. The method according to claim 14, wherein the affinity of interaction is within the range of Kd 10^{-3}-10^{-11} M.

16. The method according to claim 1, wherein the compound is any compound capable of binding to at least one of the at least two different proteins.

17. The method according to claim 16, wherein the compound is selected from the group comprising peptides, carbohydrates, lipids and nucleotides.

18. The method of claim 17, wherein the peptide comprises any of the amino acid sequences set forth on SEQ ID NOS: 1-10, 100, 125 or variants, or fragments of said sequences, or a combination of said sequences.

19. The method of claim 17, wherein the peptide comprises a contiguous amino acid sequence having at least 60% homology to any of the sequences set forth in SEQ ID NOS: 1-10, 100, 125, or a variant of said amino acid sequence, or a fragment of said amino acid sequence.

20. The method of claim 17, wherein the peptide comprises any of the amino acid sequences set forth in SEQ ID NOS: 11-99, 101-124, 126-146 or variants, or fragments of said sequences, or a combination of said sequences.

21. The method of claim 17, wherein the peptide encompasses a sequence of at least 6 to 16 contiguous amino acids capable of forming a strand-loop-strand fold.

22. A method of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and another of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein said binding site is essentially consisting of one or more "strand-loop-strand" structural motifs, comprising

iii) providing a compound capable of interacting with the receptor and/or polypeptide thereby interfering with said receptor and said polypeptide interaction,

iv) presenting the compound of step (i) to the at least two different proteins.

23. The method according to claim 22, wherein the binding site consisting of one or more "strand-loop-strand" structural motifs.

24. The method according to claims 22 or 23 further comprising at least one feature any of the claims 1-21.

25. A screening method for a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the at least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising

i) providing the at least two different proteins;

ii) providing a candidate compound;

iii) presenting the candidate compound of (ii) to the at least two different proteins of (i);

iv) determining the interaction between the at least two different proteins before and after the presenting the candidate compound to said proteins;

v) determining whether the interaction between the at least two different proteins has been modulated by the presented compound,

vi) selecting a compound capable of modulating the interaction between the at least two different proteins.

26. The screening method according to claim 25, wherein the functional cell-surface receptor is selected from the group as defined in claims 4-5.

27. The screening method according to claim 25, wherein the polypeptide is selected from the group comprising polypeptides as defined in any of the claims 6-13.

28. The screening method according to claim 27, wherein the polypeptide, is NCAM having the amino acid sequence set forth in Swiss-Prot Seq Nos: P13591,

P13595-01 or P13595, or fragments, or variants thereof, a functional homologue of NCAM.

29. The screening method according to claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of normal, degenerated or damaged NCAM presenting cells.

30. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament treatment of diseases and conditions of the central and peripheral nervous system, or of the muscles or of various organs.

31. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, impaired myelination of nerve fibers, postischaemic damage, e.g. resulting from a stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, dementias such as multiinfarct dementia, sclerosis, nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuro-muscular transmission, and schizophrenia, mood disorders, such as manic depression; for treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as after organ transplantation, or such as genetic or traumatic atrophic muscle disorders; or for treatment of diseases or conditions of various organs, such as degenerative conditions of the gonads, of the pancreas such as diabetes mellitus type I and II, of the kidney such as nephrosis and of the heart, liver and bowel.

32. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of postoperative nerve damage, traumatic nerve damage, impaired myelination of nerve fibers, postischaemic, e.g. resulting from a stroke, Parkinson's disease, Alzheimer's disease, Huntington's disease, dementias such as multiinfarct dementia, sclerosis, nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuro-muscular transmission, and schizophrenia, mood disorders, such as manic depression.

33. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the promotion of wound-healing.

34. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the treatment of cancer.

35. The screening method according to claim 31, wherein the cancer is any type of solid tumors requiring neoangiogenesis.

36. The screening method according to the claims 25-28, wherein the first compound is for the manufacture of a medicament for the prevention of cell death of heart muscle cells, such as after acute myocardial infarction, or after angiogenesis.

37. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for revascularsation.

38. The screening method according to the claims 25-28, wherein the compound is for the manufacture of a medicament for the stimulation of the ability to learn and/or the short and/or long-term memory.

39. An assay for sequential screening of a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of

i) providing the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or

fragments, or variants, or homologues of said sequences, or a fragments or a variants of said homologues,

ii) presenting the at least one receptor molecule of step (i) to the at least one polypeptide of step (i), or presenting the at least one polypeptide of step (i) to the at least one receptor molecule of step (i) and permitting the interaction between the said receptor and said polypeptide, followed by the

iii) recording the interaction between the molecules of step (ii),

iv) presenting the candidate compound to the molecules of step (ii);

v) recording the interaction between the molecules of step (iv), followed by the

vi) assessment of at least one effect of the candidate compound on the interaction between the molecules of step (iv), followed by the

vii) selection of a compound capable of modulating the interaction between the at least one functional cell-surface receptor molecule and the at least one polypeptide of step (i).

40. The assay according to claim 39, wherein step (vii) is followed by the steps of

viii) presenting the selected in step (vii) candidate compound to at least one cell presenting the at least one functional cell-surface receptor molecule, or a fragment, or a variant thereof, and the at least one polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragments or a variants of said homologues with, and

ix) assessing at least one effect of the compound on the cell of step (viii).

41. The assay according to claims 39 and 40, wherein the recording of interaction between the molecules on step (iii) or step (v), and the assessment of the at least one effect of the candidate compound on step (vi) is achieved by using a method selected from the group comprising surface plasmon resonance, nucleic magnetic resonance, sedimentation, immunoprecipitation, two-hybrid system, or resonance energy transfer.

42. The assay according to claim 40, wherein the at least one effect of step (ix) is being selected from stimulation/inhibition of receptor phosphorylation, intracellu-

lar signal transduction, gene expression, cellular adhesion, cell motility, neuritogenesis, apoptosis, cell proliferation or synaptic plasticity.

43. A method for molecular design for a compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues comprising using structural data on the binding site of NCAM with FGFR.

44. A method for isolating a candidate compound capable of modulating the interaction between at least two different proteins, wherein one of the least two different proteins is represented by a functional cell-surface receptor, or a fragment, or a variant thereof, and the other of the at least two different proteins is represented by a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues, comprising the steps of

i) providing a method for sequential screening the candidate compound as defined in claim 39 and/or

ii) providing a method for molecular design of the candidate compound as defined in claim 43,

iii) isolating the candidate compound.

45. A peptide fragment having any of the following amino acid sequences:
NIEVWVEAENALGKKV (SEQ ID NO: 2),
ATNRQGKVKAFAHL (SEQ ID NO: 3),
RYVELYVVADSQEFQK (SEQ ID NO: 4),
VAENSRGKNVAKG (SEQ ID NO: 5),
GEYWCVAENQYGQR (SEQ ID NO: 6),
RLAALNGKGLGEIS (SEQ ID NO: 7),
KYIAENMKAQNVAKEI (SEQ ID NO: 8),

TIMGLKPETRYAVR (SEQ ID NO: 9),
KGLGEISAATEFKT (SEQ ID NO: 10),
NMGIWVQAENALG (SEQ ID NO: 11),
IWVQAENMLG (SEQ ID NO: 12),
EIWVEATNRLG (SEQ ID NO: 13),
VWVQAANALG (SEQ ID NO: 14),
EVWIEKDPAKGRI (SEQ ID NO: 15),
ATNKGGEVKKNGHL (SEQ ID NO: 16),
KYVELYLVADYLEFQK (SEQ ID NO: 17),
RYVELYVVVDNAEFQ (SEQ ID NO: 18),
KYVELVIVADNREFQR (SEQ ID NO: 19),
KYIEYYLVLDNGEFKR (SEQ ID NO: 20),
RYLELYIVADHTLF (SEQ ID NO: 21),
KYVEMFVVVNHQRFQ (SEQ ID NO: 22),
RYVELFIVVDKERY (SEQ ID NO: 23),
KYVELFIVADDTVYRR (SEQ ID NO: 24),
KFIELFVVADEYVYRR (SEQ ID NO: 25),
KIVEKVIVADNSEVRK (SEQ ID NO: 26),
VELVIVADHSEAQK (SEQ ID NO: 27),
VAENSRGKNIAKG (SEQ ID NO: 28),
IAENSRGKNVARG (SEQ ID NO: 29),
AENSRGKNSFRG (SEQ ID NO: 30),
IASNLRGRNLAKG (SEQ ID NO: 31),
IPENSLGKTYAKG (SEQ ID NO: 32),
IAENMKAQNEAK (SEQ ID NO: 33),
QFIAENMKSHNETKEV (SEQ ID NO: 34),
GEYWCVAKNRVGQ (SEQ ID NO: 35),
GSYTCVAENMVGK (SEQ ID NO: 36),
GKYVCVGTNMVGER (SEQ ID NO: 37),
GNYTCVVENEYG (SEQ ID NO: 38),
GEYTCLAGNSIG (SEQ ID NO: 39),
QYYCVAENGYG (SEQ ID NO: 40),
GEYYQEAEQNGYG (SEQ ID NO: 41),
GNYTCLVENEYG (SEQ ID NO: 42),
GMYQCLAENAYG (SEQ ID NO: 43),

GMYQCAENTHG (SEQ ID NO: 44),
GIYYCLASNNYG (SEQ ID NO: 45),
GGYYCTADNSYG (SEQ ID NO: 46),
GEYQCFARNDYG (SEQ ID NO: 47),
GEYFCLASNKMG (SEQ ID NO: 48),
GEYQCFARNKFG (SEQ ID NO: 49),
GEYFCLASNKMG (SEQ ID NO: 50),
GGYYCTADNNYG (SEQ ID NO: 51),
GNYSCEAENAWGTK (SEQ ID NO: 52),
GEYTCLAENSLG (SEQ ID NO: 53),
GEYECVAENGRLG (SEQ ID NO: 54),
GNYTCVVENKFGR (SEQ ID NO: 55),
GEYTCLAGNSIG (SEQ ID NO: 56),
GEYFCVASNPIG (SEQ ID NO: 57),
EYTCIANNQAGE (SEQ ID NO: 58),
GMYQCVAENKHLG (SEQ ID NO: 59),
GEYMCTASNTIGQ (SEQ ID NO: 60),
EYVCIAENKAGEQ (SEQ ID NO: 61),
GDYTLIAKNEYGK (SEQ ID NO: 62),
GFYQCVAENEAG (SEQ ID NO: 63),
GKYECVATNSAGTR (SEQ ID NO: 64),
GEYFCVYNNSLG (SEQ ID NO: 65),
GEYECAATNAHGR (SEQ ID NO: 66),
GAYWCQGTNSVGK (SEQ ID NO: 67),
GTYSCVAENILG (SEQ ID NO: 68),
RVAAVNGKGQGDYS (SEQ ID NO: 69),
RVAAINGCGIGPFS (SEQ ID NO: 70),
AVLNGKGLG (SEQ ID NO: 71),
ALNGQGLGATS (SEQ ID NO: 72),
RLAAKNRAGLGE (SEQ ID NO: 73),
RLGVVTGKDLGEI (SEQ ID NO: 74),
TVTGLKPETSYMVK (SEQ ID NO: 75),
TLTGLKPSTRYRI (SEQ ID NO: 76),
TLTGLQPSTRYRV (SEQ ID NO: 77),
TLLGLKPDTTYDIK (SEQ ID NO: 78),

TLQGLRPETAYELR (SEQ ID NO: 79),
TLRGLRPETAYELR (SEQ ID NO: 80),
TLMNLRPKTGYSVR (SEQ ID NO: 81),
TVSGLKPGTRY (SEQ ID NO: 82),
TISGLKPDTTY (SEQ ID NO: 83),
TLQGLKPDTAY (SEQ ID NO: 84),
LRGLKPWTQYAV (SEQ ID NO: 85),
IDGLEPDTEYIVR (SEQ ID NO: 86),
LQGLKPWTQYAI (SEQ ID NO: 87),
TITGLEPGTEYTIQ (SEQ ID NO: 88),
GLKPWTQYAV (SEQ ID NO: 89),
TLASLKPWTQYAV (SEQ ID NO: 90),
LMGLQPATEYIV (SEQ ID NO: 91),
KGMGPMSEAVQFRT (SEQ ID NO: 92),
TLTGLKPDTTYDVK (SEQ ID NO: 93),
ISGLQPETSYSL (SEQ ID NO: 94),
TLLGLKPDTTYDIK (SEQ ID NO: 95),
TISGLTPETTYSI (SEQ ID NO: 96),
GNYSCLAENRLGR (SEQ ID NO: 97),
GNYTCVVENRVG (SEQ ID NO: 98),
GTYHCVATNAHG (SEQ ID NO: 99),
LSHNGVLTGYLLSY (SEQ ID NO: 100),
NGVLTGYVLRY (SEQ ID NO: 101),
NGVLTGYNLRY (SEQ ID NO: 102),
NGNLTGYLLQY (SEQ ID NO: 103),
VDENGVLTGYKIYY (SEQ ID NO: 104),
THNGALVGYSVRY (SEQ ID NO: 105),
NGILTEYILKY (SEQ ID NO: 106),
NGILIGYTLRY (SEQ ID NO: 107),
THSGQITGYKIRY (SEQ ID NO: 108),
NGKITGYIIYY (SEQ ID NO: 109),
LSHNGIFTLY (SEQ ID NO: 110),
NGILTEYTLKY (SEQ ID NO: 111),
LDPNGIITQYEISY (SEQ ID NO: 112),
NGKITGYIIYY (SEQ ID NO: 113),

HLEVQAFNGRGSGPA (SEQ ID NO: 114),
HLTVRAYNGAGYGP (SEQ ID NO: 115),
HLSVKAYNSAGTGPS (SEQ ID NO: 116),
HLAVKAYNSAGTGPS (SEQ ID NO: 117),
NLEVRAFNSAGDGP (SEQ ID NO: 118),
HLTVLAYNSKGAGP (SEQ ID NO: 119),
LRVLVFNGRGDGP (SEQ ID NO: 120),
HIDVSAFNSAGYGP (SEQ ID NO: 121),
HLAVELFNGR (SEQ ID NO: 122),
LELQSINFLGGQPA (SEQ ID NO: 123),
HFTVRAYNGAGYGP (SEQ ID NO: 124),
HLEVQAFNGRGSQPA (SEQ ID NO: 125),
VIADQPTFVKYLIK (SEQ ID NO: 126),
TIKGLRPGVVYEGQ (SEQ ID NO: 127),
TLTELSPSTQYTVK (SEQ ID NO: 128),
TLDDLAPDTTYLVQ (SEQ ID NO: 129),
TVSDVTPHAIYTVR (SEQ ID NO: 130),
IIRGLNASTRYLFR (SEQ ID NO:131),
TLMNLRPKTGYSVR (SEQ ID NO:132),
TLTGLKPGTEYEVR (SEQ ID NO: 133),
GPEHLMPSSTYVAR (SEQ ID NO: 134),
RVTGLTPKKTYEFR (SEQ ID NO: 135),
LTGLKPGTEYEFR (SEQ ID NO: 136),
EVRVQAVNGGGNGPP (SEQ ID NO: 137),
LIKVVAINDRGE (SEQ ID NO: 138),
VVSIIAVNGREE (SEQ ID NO: 139),
VVSVYAQNQNGE (SEQ ID NO: 140),
TISLVAEKGRHK (SEQ ID NO: 141),
HLEVQAFNGRGSGPA (SEQ ID NO: 142),
HVEVQAFNGRGLGPA (SEQ ID NO: 143),
HVEVQAFNGRGLGPA (SEQ ID NO: 144),
EFRVRAVNGAGEG (SEQ ID NO: 145),
VARVRTRLAPGSRLS (SEQ ID NO: 146)
or fragments, or variants thereof.

46. A compound comprising at least one peptide fragment having at least one of the sequences set forth in SEQ ID NO: 2-146 or a fragment, or variant, or homologue of said sequences.

47. Use of a peptide fragment as defined in claim 45 and/or compound as defined in claim 46 for the manufacture of a medicament for treatment of conditions as defined in any of the claims 29-38.

48. An antibody capable of binding to an epitope comprising a binding site to a cell surface receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or a fragment or a variant of said antibody.

49. An antibody capable of binding to an epitope comprising at least one of the sequences set forth in SEQ ID NOS: 1-146, or a fragment, or a variant of said antibody.

50. Use of an antibody according to claims 48 or 49 for modulating the interaction between a cell surface receptor, or a fragment or variant thereof, and a polypeptide having a binding site to said receptor, wherein at least a part of said binding site comprises at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues.

51. Use of an antibody as defined in claims 48 or 49 for the manufacture of a medicament for treatment of conditions as defined in any of the claims 29-38.

52. Use of an antibody as defined in claims 48 or 49 for determining the presence of a substance comprising an epitope comprising at least one of the sequences set forth in SEQ ID NOS: 1-146, or fragments, or variants, or homologues of said sequences, or fragments or variants of said homologues in a sample.

53. A method for the production of an antibody as defined in claims 48 and/or 49 comprising administering to an animal a peptide fragment comprising at least one sequence selected from the sequences set forth in SEQ ID NOS: 1-146.

54. A method for producing a pharmaceutical composition comprising the steps of clam 39 and further the step of formulating the compound with pharmaceutically acceptable carrier or solvent.

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